

SEQUENCE LISTING

<110> Shone, Clifford Charles
Sutton, John Mark

<120> Targeted Agents for Nerve Regeneration

<130> MSQ01-003-US

<140> 10/521,401

<141> 2005-09-12

<150> GB 0216865.6

<151> 2002-07-19

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

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Ile Glu Gly Arg Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile
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Asp Gln Ala Lys Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu
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Ser Lys Ser Glu Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser
35 40 45

Glu Ile Asn Gly Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe
50 55 60

Pro Ser Asn Leu Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn
65 70 75 80

Lys Met Lys Thr Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro
85 90 95

Ala Tyr Leu Gly Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly
100 105 110

Thr Ile Asn Lys Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn
115 120 125

Lys Asp Arg Leu Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val
130 135 140

Ser Gln Phe Ala Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys
 145 150 155 160

Gly Ser Lys Ala Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln
 165 170 175

Leu Glu Met Leu Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met
 180 185 190

Arg Leu Ser Ser Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met
 195 200 205

Gly Thr Ala Ile Asn Pro Lys
 210 215

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Asn Ser Leu Ile Lys Ser Ala Lys Tyr Ser Ser Lys Asp Lys Met Ala
 20 25 30

Ile Tyr Asn Tyr Thr Lys Asn Ser Ser Pro Ile Asn Thr Pro Leu Arg
 35 40 45

Ser Ala Asn Gly Asp Val Asn Lys Leu Ser Glu Asn Ile Gln Glu Gln
 50 55 60

Val Arg Gln Leu Asp Ser Thr Ile Ser Lys Ser Val Thr Pro Asp Ser
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser Ser Ile Thr
 85 90 95

Gly Phe Thr Arg Glu Asp Leu His Met Leu Gln Gln Thr Asn Asn Gly
 100 105 110

Gln Tyr Asn Glu Ala Leu Val Ser Lys Leu Asn Asn Leu Met Asn Ser
 115 120 125

Arg Ile Tyr Arg Glu Asn Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly
 130 135 140

Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Glu Leu Pro Lys
145 150 155 160

Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Glu Leu Thr Ala Tyr Pro
165 170 175

Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly
180 185 190

Ser Val Lys Leu Ser Asp Asn Lys Arg Lys Ile Ile Ile Thr Ala Val
195 200 205

Val Phe Lys Lys
210

<210> 3
<211> 636
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic

<400> 3

Gly Cys Thr Gly Ala Ala Ala Cys Cys Ala Ala Ala Ala Cys Thr
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Thr Cys Ala Cys Cys Gly Ala Cys Cys Thr Gly Gly Thr Thr Gly Ala
20 25 30

Ala Gly Cys Thr Ala Cys Cys Ala Ala Ala Thr Gly Gly Gly Gly Thr
35 40 45

Ala Ala Cys Thr Cys Thr Cys Thr Gly Ala Thr Cys Ala Ala Ala Thr
50 55 60

Cys Thr Gly Cys Thr Ala Ala Ala Thr Ala Cys Thr Cys Thr Thr Cys
65 70 75 80

Thr Ala Ala Ala Gly Ala Cys Ala Ala Ala Ala Thr Gly Gly Cys Thr
85 90 95

Ala Thr Cys Thr Ala Cys Ala Ala Cys Thr Ala Cys Ala Cys Cys Ala
100 105 110

Ala Ala Ala Ala Cys Thr Cys Thr Thr Cys Thr Cys Cys Gly Ala Thr
115 120 125

Cys Ala Ala Cys Ala Cys Cys Cys Cys Gly Cys Thr Gly Cys Gly Thr

130	135	140
Thr Cys Thr Gly Cys	Thr Ala Ala Cys Gly	Gly Thr Gly Ala Cys Gly
145	150	155
Thr Thr Ala Ala Cys	Ala Ala Ala Cys Thr Gly	Thr Cys Thr Gly Ala
165	170	175
Ala Ala Ala Cys	Ala Thr Cys Cys Ala	Gly Gly Ala Ala Cys Ala Gly
180	185	190
Gly Thr Thr Cys Gly	Thr Cys Ala Gly Cys Thr Gly	Gly Ala Cys Thr
195	200	205
Cys Thr Ala Cys Cys	Ala Thr Cys Thr Cys Thr	Ala Ala Ala Thr Cys
210	215	220
Thr Gly Thr Thr Ala	Cys Cys Cys Gly Gly	Ala Cys Thr Cys Thr
225	230	235
Gly Thr Thr Thr Ala	Cys Gly Thr Thr Thr	Ala Cys Cys Gly Thr Cys
245	250	255
Thr Gly Cys Thr Gly	Ala Ala Cys Cys Thr Gly	Gly Ala Cys Thr Ala
260	265	270
Cys Cys Thr Gly Thr	Cys Thr Thr Cys Thr Ala	Thr Cys Ala Cys Cys
275	280	285
Gly Gly Thr Thr Thr	Cys Ala Cys Cys Cys Gly	Thr Gly Ala Ala Gly
290	295	300
Ala Cys Cys Thr Gly	Cys Ala Cys Ala Thr Gly	Cys Thr Gly Cys Ala
305	310	315
Gly Cys Ala Gly Ala	Cys Cys Ala Ala Cys	Ala Ala Cys Gly Gly Thr
325	330	335
Cys Ala Gly Thr Ala	Cys Ala Ala Cys Gly	Ala Ala Gly Cys Thr Cys
340	345	350
Thr Gly Gly Thr Thr	Thr Cys Thr Ala Ala	Ala Cys Thr Gly Ala Ala
355	360	365
Cys Ala Ala Cys Cys	Thr Gly Ala Ala Cys	Thr Cys Thr Cys Thr
370	375	380
Cys Gly Thr Ala Thr	Cys Thr Ala Cys Cys	Gly Thr Gly Ala Ala Ala

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385          390          395          400
Ala Cys Gly Gly Thr Thr Ala Cys Thr Cys Thr Thr Cys Thr Ala Cys
      405          410          415
Cys Cys Ala Gly Cys Thr Gly Gly Thr Thr Thr Cys Thr Gly Gly Thr
      420          425          430
Gly Cys Thr Gly Cys Thr Cys Thr Gly Gly Cys Thr Gly Gly Thr Cys
      435          440          445
Gly Thr Cys Cys Gly Ala Thr Cys Gly Ala Ala Cys Thr Gly Ala Ala
      450          455          460
Ala Cys Thr Gly Gly Ala Ala Cys Thr Gly Cys Cys Gly Ala Ala Ala
      465          470          475          480
Gly Gly Thr Ala Cys Cys Ala Ala Ala Gly Cys Thr Gly Cys Thr Thr
      485          490          495
Ala Cys Ala Thr Cys Gly Ala Cys Thr Cys Thr Ala Ala Ala Gly Ala
      500          505          510
Ala Cys Thr Gly Ala Cys Cys Gly Cys Thr Thr Ala Cys Cys Cys Cys
      515          520          525
Gly Gly Thr Cys Ala Gly Cys Ala Gly Gly Ala Ala Gly Thr Thr Cys
      530          535          540
Thr Gly Cys Thr Gly Cys Cys Gly Cys Gly Thr Gly Gly Thr Ala Cys
      545          550          555          560
Cys Gly Ala Ala Thr Ala Cys Gly Cys Thr Gly Thr Thr Gly Gly Thr
      565          570          575
Thr Cys Thr Gly Thr Thr Ala Ala Ala Cys Thr Gly Thr Cys Thr Gly
      580          585          590
Ala Cys Ala Ala Cys Ala Ala Ala Cys Gly Thr Ala Ala Ala Ala Thr
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Cys Ala Thr Cys Ala Thr Cys Ala Cys Cys Gly Cys Thr Gly Thr Thr
      610          615          620
Gly Thr Thr Thr Thr Cys Ala Ala Gly Ala Ala Gly
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<210> 4

<211> 212
 <212> PRT
 <213> Staphylococcus aureus
 <400> 4

Ala Asp Val Lys Asn Phe Thr Asp Leu Asp Glu Ala Thr Lys Trp Gly
 1 5 10 15

Asn Lys Leu Ile Lys Gln Ala Lys Tyr Ser Ser Asp Asp Lys Ile Ala
 20 25 30

Leu Tyr Glu Tyr Thr Lys Asp Ser Ser Lys Ile Asn Gly Pro Leu Arg
 35 40 45

Leu Ala Gly Gly Asp Ile Asn Lys Leu Asp Ser Thr Thr Gln Asp Lys
 50 55 60

Val Arg Arg Leu Asp Ser Ser Ile Ser Lys Ser Thr Thr Pro Glu Ser
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Thr Ser Ile Val
 85 90 95

Gly Phe Thr Asn Glu Asp Leu Tyr Lys Leu Gln Gln Thr Asn Asn Gly
 100 105 110

Gln Tyr Asp Glu Asn Leu Val Arg Lys Leu Asn Asn Val Met Asn Ser
 115 120 125

Arg Ile Tyr Arg Glu Asp Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly
 130 135 140

Ala Ala Val Gly Gly Arg Pro Ile Glu Leu Arg Leu Glu Leu Pro Lys
 145 150 155 160

Gly Thr Lys Ala Ala Tyr Leu Asn Ser Lys Asp Leu Thr Ala Tyr Tyr
 165 170 175

Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly
 180 185 190

Ser Val Glu Leu Ser Asn Asp Lys Lys Lys Ile Ile Ile Thr Ala Ile
 195 200 205

Val Phe Lys Lys
 210

<210> 5
 <211> 247
 <212> PRT

<213> Staphylococcus aureus

<400> 5

Met Lys Arg Lys Leu Phe Phe Lys Ile Ile Phe Val Leu Ser Leu Val
1 5 10 15

Leu Ser Ile His Ser Ile Asn Asp Arg Thr Thr Glu Leu Ser Asn Ile
20 25 30

Ala Leu Ala Asp Asp Val Lys Asn Phe Thr Asp Leu Thr Glu Ala Thr
35 40 45

Asn Trp Gly Asn Lys Leu Ile Lys Gln Ala Asn Tyr Ser Ser Lys Asp
50 55 60

Lys Glu Ala Ile Tyr Asn Tyr Thr Lys Tyr Ser Ser Pro Ile Asn Thr
65 70 75 80

Pro Leu Arg Ser Ser Gln Gly Asp Ile Ser Asn Phe Ser Ala Asp Leu
85 90 95

Gln Glu Lys Ile Leu Arg Leu Asp Arg Leu Ile Ser Lys Ser Ser Thr
100 105 110

Ser Asp Ser Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser
115 120 125

Ser Val Lys Gly Phe Ser Ser Glu Asp Leu Glu Leu Leu Tyr Lys Thr
130 135 140

Glu Asn Gly Lys Tyr Asn Glu Glu Leu Val Lys Lys Leu Asn Asn Ile
145 150 155 160

Met Asn Ser Lys Ile Tyr Thr Glu Tyr Gly Tyr Ser Ser Thr Gln Leu
165 170 175

Val Lys Gly Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Gln
180 185 190

Leu Pro Lys Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Asn Leu Thr
195 200 205

Ala Tyr Pro Gly Gln Gln Glu Ile Leu Leu Pro Arg Gly Thr Asp Tyr
210 215 220

Thr Ile Asn Thr Val Lys Leu Ser Asp Asp His Lys Arg Ile Leu Ile
225 230 235 240

Glu Gly Ile Val Phe Lys Lys

245

<210> 6
 <211> 211
 <212> PRT
 <213> Clostridium limosum
 <400> 6

Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys
 1 5 10 15

Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu
 20 25 30

Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly
 35 40 45

Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu
 50 55 60

Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr
 65 70 75 80

Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly
 85 90 95

Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys
 100 105 110

Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu
 115 120 125

Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala
 130 135 140

Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala
 145 150 155 160

Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu
 165 170 175

Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser
 180 185 190

Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile
 195 200 205

Asn Pro Lys
 210

<210> 7
 <211> 160
 <212> PRT
 <213> *Listeria monocytogenes*
 <400> 7

Asn Lys Ser Leu Lys Phe Thr Ser Leu Glu Glu Ser Glu Lys Trp Gly
 1 5 10 15

Ile Asp Gly Phe Ser Val Trp Arg Asn Ser Leu Ser Ser Arg Glu Ile
 20 25 30

Gln Ala Ile Arg Asp Tyr Thr Asp Ile Trp His Tyr Gly Asn Met Asn
 35 40 45

Gly Tyr Leu Arg Gly Ser Val Glu Lys Leu Ala Pro Asp Asn Ala Glu
 50 55 60

Arg Ile Lys Asn Leu Ser Ser Ala Leu Glu Lys Ala Glu Leu Pro Asp
 65 70 75 80

Asn Ile Ile Leu Tyr Arg Gly Thr Ser Ser Glu Ile Leu Asp Asn Phe
 85 90 95

Leu Asp Leu Lys Asn Leu Asn Tyr Gln Asn Leu Val Gly Lys Thr Ile
 100 105 110

Glu Glu Lys Gly Phe Met Ser Thr Thr Thr Ile Ser Asn Gln Thr Phe
 115 120 125

Ser Gly Asn Val Thr Met Lys Ile Asn Ala Pro Lys Gly Ser Lys Gly
 130 135 140

Ala Tyr Leu Ala His Phe Ser Glu Thr Pro Glu Glu Ala Glu Val Leu
 145 150 155 160

<210> 8
 <211> 175
 <212> PRT
 <213> *Clostridium acetobutylicum*
 <400> 8

Thr Asn Met Asp Gln Ala Asn Glu Trp Gly Ser Gln Tyr Tyr Asp Asn
 1 5 10 15

Trp Leu Lys Ser Leu Asn Asp Ser Glu Arg Asn Ala Ile Arg Gln Tyr
 20 25 30

Thr Gly Asn Asp Tyr Lys Lys Ile Asn Asn Tyr Leu Arg Gly Val Asn
 35 40 45

Asp Ser Leu Asp Gly Ile Asp Pro Lys Ile Ile Glu Asp Ile Lys Ser
50 55 60

Gly Leu Lys Lys Ala Ser Val Pro His Asp Met Lys Val Tyr Arg Gly
65 70 75 80

Thr Asp Leu Asn Pro Leu Arg Asn Leu Ile Asp Val Gly Lys Asp Gly
85 90 95

Ser Leu Asp Phe Ser Leu Val Gly Lys Thr Phe Lys Asp Asp Gly Phe
100 105 110

Met Ser Thr Ala Leu Val Lys Glu Ser Ser Phe Asp Tyr Met Asn Val
115 120 125

Ser Trp Glu Ile Asn Val Pro Lys Gly Thr Glu Ala Ala Tyr Val Ser
130 135 140

Lys Ile Ser Tyr Phe Pro Asp Glu Ala Glu Leu Leu Leu Asn His Gly
145 150 155 160

Gln Glu Met Ile Ile Lys Glu Ala Thr Val Gly Ser Asp Gly Lys
165 170 175

<210> 9
<211> 250
<212> PRT
<213> Streptococcus pyogenes
<400> 9

Met Leu Lys Lys Arg Tyr Gln Leu Ala Ile Val Leu Leu Leu Ser Cys
1 5 10 15

Phe Ser Leu Ile Trp Gln Thr Glu Gly Leu Val Glu Leu Phe Val Cys
20 25 30

Glu His Tyr Glu Arg Ala Val Cys Glu Gly Thr Pro Ala Tyr Phe Thr
35 40 45

Phe Ser Asp Gln Lys Gly Ala Glu Thr Leu Ile Lys Lys Arg Trp Gly
50 55 60

Lys Gly Leu Ile Tyr Pro Arg Ala Glu Gln Glu Ala Met Ala Ala Tyr
65 70 75 80

Thr Cys Gln Gln Ala Gly Pro Ile Asn Thr Ser Leu Asp Lys Ala Lys
85 90 95

Gly Glu Leu Ser Gln Leu Thr Pro Glu Leu Arg Asp Gln Val Ala Gln

100 105 110
 Leu Asp Ala Ala Thr His Arg Leu Val Ile Pro Trp Asn Ile Val Val
 115 120 125
 Tyr Arg Tyr Val Tyr Glu Thr Phe Leu Arg Asp Ile Gly Val Ser His
 130 135 140
 Ala Asp Leu Thr Ser Tyr Tyr Arg Asn His Gln Phe Asp Pro His Ile
 145 150 155 160
 Leu Cys Lys Ile Lys Leu Gly Thr Arg Tyr Thr Lys His Ser Phe Met
 165 170 175
 Ser Thr Thr Ala Leu Lys Asn Gly Ala Met Thr His Arg Pro Val Glu
 180 185 190
 Val Arg Ile Cys Val Lys Lys Gly Ala Lys Ala Ala Phe Val Glu Pro
 195 200 205
 Tyr Ser Ala Val Pro Ser Glu Val Glu Leu Leu Phe Pro Arg Gly Cys
 210 215 220
 Gln Leu Glu Val Val Gly Ala Tyr Val Ser Gln Asp Gln Lys Lys Leu
 225 230 235 240
 His Ile Glu Ala Tyr Phe Lys Gly Ser Leu
 245 250

<210> 10
 <211> 250
 <212> PRT
 <213> Streptococcus pyogenes
 <400> 10

Met Leu Lys Lys Arg Tyr Gln Leu Ala Ile Val Leu Leu Leu Ser Cys
 1 5 10 15
 Phe Ser Leu Ile Trp Gln Thr Glu Gly Leu Val Glu Leu Phe Val Cys
 20 25 30
 Glu His Tyr Glu Arg Ala Val Cys Glu Gly Thr Pro Ala Tyr Phe Thr
 35 40 45
 Phe Ser Asp Gln Lys Gly Ala Glu Thr Leu Ile Lys Lys Arg Trp Gly
 50 55 60
 Lys Gly Leu Ile Tyr Pro Arg Ala Glu Gln Glu Ala Met Ala Ala Tyr
 65 70 75 80

Thr Cys Gln Gln Ala Gly Pro Ile Asn Thr Ser Leu Asp Lys Ala Lys
85 90 95

Gly Glu Leu Ser Gln Leu Thr Pro Glu Leu Arg Asp Gln Val Ala Gln
100 105 110

Leu Asp Ala Ala Thr His Arg Leu Val Ile Pro Trp Asn Ile Val Val
115 120 125

Tyr Arg Tyr Val Tyr Glu Thr Phe Leu Arg Asp Ile Gly Val Ser His
130 135 140

Ala Asp Leu Thr Ser Tyr Tyr Arg Asn His Gln Phe Asp Pro His Ile
145 150 155 160

Leu Cys Lys Ile Lys Leu Gly Thr Arg Tyr Thr Lys His Ser Phe Met
165 170 175

Ser Thr Thr Ala Leu Lys Asn Gly Ala Met Thr His Arg Pro Val Glu
180 185 190

Val Arg Ile Cys Val Lys Lys Gly Ala Lys Ala Ala Phe Val Glu Pro
195 200 205

Tyr Ser Ala Val Pro Ser Glu Val Glu Leu Leu Phe Pro Arg Gly Cys
210 215 220

Gln Leu Glu Val Val Gly Ala Tyr Val Ser Gln Asp Gln Lys Lys Leu
225 230 235 240

His Ile Glu Ala Tyr Phe Lys Gly Ser Leu
245 250

<210> 11

<211> 855

<212> PRT

<213> Clostridium botulinum

<400> 11

Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp
1 5 10 15

Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro Phe Ile Gly Asp
20 25 30

Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys Asp Ile Asn Glu
35 40 45

Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser Val Asp Gln Val

50	55	60
Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu Asp Leu Leu Tyr 65 70 75 80		
Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly Glu Asn Gln Val 85 90 95		
Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu Asn Ser Tyr Tyr 100 105 110		
Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu Asp Phe Thr Phe 115 120 125		
Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala Lys Val Tyr Thr 130 135 140		
Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly Val Gln Gly Gly 145 150 155 160		
Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp Phe Thr Thr Asn 165 170 175		
Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp Val Ser Ala Ile 180 185 190		
Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn Ser Val Arg Arg 195 200 205		
Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val Thr Ile Leu Leu 210 215 220		
Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Ala Phe Val Ile 225 230 235 240		
Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys Thr Ile Asp Asn 245 250 255		
Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser Tyr Glu Trp Met 260 265 270		
Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe Asn Asn Ile Ser 275 280 285		
Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly Ala Ile Lys Ala 290 295 300		
Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp Lys Glu Asn		

305 310 315 320
 Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp Val Lys Ile
 325 330 335
 Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu Cys Ser Val
 340 345 350
 Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp Glu Leu Asn
 355 360 365
 Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn Leu Ile Asp Ser
 370 375 380
 His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu Lys Ala Lys Val
 385 390 395 400
 Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr
 405 410 415
 Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile
 420 425 430
 Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val
 435 440 445
 Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln
 450 455 460
 Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu
 465 470 475 480
 Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn
 485 490 495
 Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys
 500 505 510
 Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn
 515 520 525
 Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr
 530 535 540
 Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp
 545 550 555 560
 Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val

				565					570					575		
Thr	Asn	Asn	Met	Met	Gly	Asn	Met	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	
			580					585					590			
Ile	Asp	Thr	Ile	Lys	Val	Lys	Glu	Leu	Thr	Gly	Ile	Asn	Phe	Ser	Lys	
		595					600					605				
Thr	Ile	Thr	Phe	Glu	Ile	Asn	Lys	Ile	Pro	Asp	Thr	Gly	Leu	Ile	Thr	
	610					615					620					
Ser	Asp	Ser	Asp	Asn	Ile	Asn	Met	Trp	Ile	Arg	Asp	Phe	Tyr	Ile	Phe	
625					630					635					640	
Ala	Lys	Glu	Leu	Asp	Gly	Lys	Asp	Ile	Asn	Ile	Leu	Phe	Asn	Ser	Leu	
				645					650					655		
Gln	Tyr	Thr	Asn	Val	Val	Lys	Asp	Tyr	Trp	Gly	Asn	Asp	Leu	Arg	Tyr	
			660					665					670			
Asn	Lys	Glu	Tyr	Tyr	Met	Val	Asn	Ile	Asp	Tyr	Leu	Asn	Arg	Tyr	Met	
		675					680					685				
Tyr	Ala	Asn	Ser	Arg	Gln	Ile	Val	Phe	Asn	Thr	Arg	Arg	Asn	Asn	Asn	
	690					695					700					
Asp	Phe	Asn	Glu	Gly	Tyr	Lys	Ile	Ile	Ile	Lys	Arg	Ile	Arg	Gly	Asn	
705					710					715					720	
Thr	Asn	Asp	Thr	Arg	Val	Arg	Gly	Gly	Asp	Ile	Leu	Tyr	Phe	Asp	Met	
				725					730					735		
Thr	Ile	Asn	Asn	Lys	Ala	Tyr	Asn	Leu	Phe	Met	Lys	Asn	Glu	Thr	Met	
			740					745					750			
Tyr	Ala	Asp	Asn	His	Ser	Thr	Glu	Asp	Ile	Tyr	Ala	Ile	Gly	Leu	Arg	
		755					760					765				
Glu	Gln	Thr	Lys	Asp	Ile	Asn	Asp	Asn	Ile	Ile	Phe	Gln	Ile	Gln	Pro	
	770					775					780					
Met	Asn	Asn	Thr	Tyr	Tyr	Tyr	Ala	Ser	Gln	Ile	Phe	Lys	Ser	Asn	Phe	
785					790					795					800	
Asn	Gly	Glu	Asn	Ile	Ser	Gly	Ile	Cys	Ser	Ile	Gly	Thr	Tyr	Arg	Phe	
				805					810					815		
Arg	Leu	Gly	Gly	Asp	Trp	Tyr	Arg	His	Asn	Tyr	Leu	Val	Pro	Thr	Val	

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 Gly Phe Val Pro Val Ser Glu
 850 855

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 <212> PRT
 <213> Clostridium botulinum
 <400> 12

 Gly Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn
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 Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn
 20 25 30

 Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp
 35 40 45

 Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu
 50 55 60

 Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp
 65 70 75 80

 Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser
 85 90 95

 Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp
 100 105 110

 Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn
 115 120 125

 Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu
 130 135 140

 Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile
 145 150 155 160

 Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr
 165 170 175

 Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile
 180 185 190

Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr
 195 200 205
 Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser
 210 215 220
 Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala
 225 230 235 240
 Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln
 245 250 255
 Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn
 260 265 270
 Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr
 275 280 285
 Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp
 290 295 300
 Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr
 305 310 315 320
 Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr
 325 330 335
 Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr
 340 345 350
 Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu
 355 360 365
 Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met
 370 375 380
 Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn
 385 390 395 400
 Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg
 405 410 415
 Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys
 420 425 430
 Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly
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Phe Val Pro Val Ser Glu
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Ala Tyr Ser Asn Thr Tyr Gln Glu Phe Thr Asn Ile Asp Gln Ala Lys
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Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu
20 25 30

Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly
35 40 45

Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu
50 55 60

Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr
65 70 75 80

Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly
85 90 95

Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys
100 105 110

Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu
115 120 125

Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala
130 135 140

Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala
145 150 155 160

Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu
165 170 175

Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser
180 185 190

Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile
195 200 205

Asn Pro Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys
 210 215 220
 Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro Phe
 225 230 235 240
 Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys Asp
 245 250 255
 Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser Val
 260 265 270
 Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu Asp
 275 280 285
 Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly Glu
 290 295 300
 Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu Asn
 305 310 315 320
 Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu Asp
 325 330 335
 Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala Lys
 340 345 350
 Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly Val
 355 360 365
 Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp Phe
 370 375 380
 Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp Val
 385 390 395 400
 Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn Ser
 405 410 415
 Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val Thr
 420 425 430
 Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Ala
 435 440 445
 Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys Thr
 450 455 460

Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser Tyr
 465 470 475 480
 Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe Asn
 485 490 495
 Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly Ala
 500 505 510
 Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp
 515 520 525
 Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp
 530 535 540
 Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu
 545 550 555 560
 Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp
 565 570 575
 Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn Leu
 580 585 590
 Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu Lys
 595 600 605
 Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe
 610 615 620
 Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe
 625 630 635 640
 Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn
 645 650 655
 Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly
 660 665 670
 Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser
 675 680 685
 Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile
 690 695 700
 Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg
 705 710 715 720

Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser
 725 730 735

Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu
 740 745 750

Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe
 755 760 765

Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe
 770 775 780

Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn
 785 790 795 800

Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn
 805 810 815

Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly
 820 825 830

Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe
 835 840 845

Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe
 850 855 860

Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp
 865 870 875 880

Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn
 885 890 895

Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg
 900 905 910

Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile
 915 920 925

Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr
 930 935 940

Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn
 945 950 955 960

Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile
 965 970 975

Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln
 980 985 990

Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys
 995 1000 1005

Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly
 1010 1015 1020

Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr
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Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu
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Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu
 1055 1060 1065

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Ile Tyr Asn Tyr Thr Lys Asn Ser Ser Pro Ile Asn Thr Pro Leu Arg
 35 40 45

Ser Ala Asn Gly Asp Val Asn Lys Leu Ser Glu Asn Ile Gln Glu Gln
 50 55 60

Val Arg Gln Leu Asp Ser Thr Ile Ser Lys Ser Val Thr Pro Asp Ser
 65 70 75 80

Val Tyr Val Tyr Arg Leu Leu Asn Leu Asp Tyr Leu Ser Ser Ile Thr
 85 90 95

Gly Phe Thr Arg Glu Asp Leu His Met Leu Gln Gln Thr Asn Asn Gly
 100 105 110

Gln Tyr Asn Glu Ala Leu Val Ser Lys Leu Asn Asn Leu Met Asn Ser

115		120		125
Arg Ile Tyr Arg Glu Asn Gly Tyr Ser Ser Thr Gln Leu Val Ser Gly	130	135	140	
Ala Ala Leu Ala Gly Arg Pro Ile Glu Leu Lys Leu Glu Leu Pro Lys	145	150	155	160
Gly Thr Lys Ala Ala Tyr Ile Asp Ser Lys Glu Leu Thr Ala Tyr Pro	165	170	175	
Gly Gln Gln Glu Val Leu Leu Pro Arg Gly Thr Glu Tyr Ala Val Gly	180	185	190	
Ser Val Lys Leu Ser Asp Asn Lys Arg Lys Ile Ile Ile Thr Ala Val	195	200	205	
Val Phe Lys Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn	210	215	220	
Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro	225	230	235	240
Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys	245	250	255	
Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser	260	265	270	
Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu	275	280	285	
Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly	290	295	300	
Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu	305	310	315	320
Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu	325	330	335	
Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala	340	345	350	
Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly	355	360	365	
Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp				

370	375	380
Phe Thr Thr Asn Ile 385	Leu Arg Lys Asp Thr 390	Leu Asp Lys Ile Ser Asp 395 400
Val Ser Ala Ile 405	Ile Pro Tyr Ile Gly 410	Pro Ala Leu Asn Ile Ser Asn 415
Ser Val Arg 420	Arg Gly Asn Phe Thr 425	Ala Phe Ala Val Thr Gly Val 430
Thr Ile Leu 435	Leu Glu Ala Phe Pro 440	Glu Phe Thr Ile Pro Ala Leu Gly 445
Ala Phe Val 450	Ile Tyr Ser Lys Val 455	Gln Glu Arg Asn Glu Ile Ile Lys 460
Thr Ile Asp Asn Cys 465	Leu Glu Gln Arg Ile 470	Lys Arg Trp Lys Asp Ser 475 480
Tyr Glu Trp Met 485	Met Gly Thr Trp Leu 490	Ser Arg Ile Ile Thr Gln Phe 495
Asn Asn Ile 500	Ser Tyr Gln Met Tyr 505	Asp Ser Leu Asn Tyr Gln Ala Gly 510
Ala Ile Lys 515	Ala Lys Ile Asp Leu 520	Glu Tyr Lys Lys Tyr Ser Gly Ser 525
Asp Lys Glu Asn Ile 530	Lys Ser Gln Val Glu 535	Asn Leu Lys Asn Ser Leu 540
Asp Val Lys Ile Ser 545	Glu Ala Met Asn Asn 550	Ile Asn Lys Phe Ile Arg 555 560
Glu Cys Ser Val 565	Thr Tyr Leu Phe Lys 570	Asn Met Leu Pro Lys Val Ile 575
Asp Glu Leu Asn Glu 580	Phe Asp Arg Asn Thr 585	Lys Ala Lys Leu Ile Asn 590
Leu Ile Asp 595	Ser His Asn Ile Ile 600	Leu Val Gly Glu Val Asp Lys Leu 605
Lys Ala Lys Val Asn Asn 610	Ser Phe Gln Asn Thr 615	Ile Pro Phe Asn Ile 620
Phe Ser Tyr Thr Asn Asn Ser 625	Leu Leu Lys Asp Ile Ile 630	Asn Glu Tyr 635

625		630		635		640									
Phe	Asn	Asn	Ile	Asn	Asp	Lys	Ile	Leu	Ser	Leu	Gln	Asn	Arg	Lys	
				645				650					655		
Asn	Thr	Leu	Val	Asp	Thr	Ser	Gly	Tyr	Asn	Ala	Glu	Val	Ser	Glu	Glu
			660					665					670		
Gly	Asp	Val	Gln	Leu	Asn	Pro	Ile	Phe	Pro	Phe	Asp	Phe	Lys	Leu	Gly
		675					680					685			
Ser	Ser	Gly	Glu	Asp	Arg	Gly	Lys	Val	Ile	Val	Thr	Gln	Asn	Glu	Asn
	690					695					700				
Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Ser	Phe	Ser	Ile	Ser	Phe	Trp	Ile
705					710					715					720
Arg	Ile	Asn	Lys	Trp	Val	Ser	Asn	Leu	Pro	Gly	Tyr	Thr	Ile	Ile	Asp
				725					730					735	
Ser	Val	Lys	Asn	Asn	Ser	Gly	Trp	Ser	Ile	Gly	Ile	Ile	Ser	Asn	Phe
			740					745					750		
Leu	Val	Phe	Thr	Leu	Lys	Gln	Asn	Glu	Asp	Ser	Glu	Gln	Ser	Ile	Asn
		755					760					765			
Phe	Ser	Tyr	Asp	Ile	Ser	Asn	Asn	Ala	Pro	Gly	Tyr	Asn	Lys	Trp	Phe
	770					775					780				
Phe	Val	Thr	Val	Thr	Asn	Asn	Met	Met	Gly	Asn	Met	Lys	Ile	Tyr	Ile
785					790					795					800
Asn	Gly	Lys	Leu	Ile	Asp	Thr	Ile	Lys	Val	Lys	Glu	Leu	Thr	Gly	Ile
				805					810					815	
Asn	Phe	Ser	Lys	Thr	Ile	Thr	Phe	Glu	Ile	Asn	Lys	Ile	Pro	Asp	Thr
			820					825					830		
Gly	Leu	Ile	Thr	Ser	Asp	Ser	Asp	Asn	Ile	Asn	Met	Trp	Ile	Arg	Asp
		835					840					845			
Phe	Tyr	Ile	Phe	Ala	Lys	Glu	Leu	Asp	Gly	Lys	Asp	Ile	Asn	Ile	Leu
	850					855					860				
Phe	Asn	Ser	Leu	Gln	Tyr	Thr	Asn	Val	Val	Lys	Asp	Tyr	Trp	Gly	Asn
865					870					875					880
Asp	Leu	Arg	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Val	Asn	Ile	Asp	Tyr	Leu

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      885              890              895
Asn Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg
      900              905              910

Arg Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg
      915              920              925

Ile Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu
      930              935              940

Tyr Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys
      945              950              955              960

Asn Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala
      965              970              975

Ile Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe
      980              985              990

Gln Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe
      995              1000              1005

Lys Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile
      1010              1015              1020

Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn
      1025              1030              1035

Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu
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Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu
      1055              1060              1065

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Ala Trp Gly Asn Ala Gln Tyr Lys Lys Tyr Gly Leu Ser Lys Ser Glu
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Lys Glu Ala Ile Val Ser Tyr Thr Lys Ser Ala Ser Glu Ile Asn Gly
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 Lys Leu Arg Gln Asn Lys Gly Val Ile Asn Gly Phe Pro Ser Asn Leu
 50 55 60
 Ile Lys Gln Val Glu Leu Leu Asp Lys Ser Phe Asn Lys Met Lys Thr
 65 70 75 80
 Pro Glu Asn Ile Met Leu Phe Arg Gly Asp Asp Pro Ala Tyr Leu Gly
 85 90 95
 Thr Glu Phe Gln Asn Thr Leu Leu Asn Ser Asn Gly Thr Ile Asn Lys
 100 105 110
 Thr Ala Phe Glu Lys Ala Lys Ala Lys Phe Leu Asn Lys Asp Arg Leu
 115 120 125
 Glu Tyr Gly Tyr Ile Ser Thr Ser Leu Met Asn Val Ser Gln Phe Ala
 130 135 140
 Gly Arg Pro Ile Ile Thr Lys Phe Lys Val Ala Lys Gly Ser Lys Ala
 145 150 155 160
 Gly Tyr Ile Asp Pro Ile Ser Ala Phe Ala Gly Gln Leu Glu Met Leu
 165 170 175
 Leu Pro Arg His Ser Thr Tyr His Ile Asp Asp Met Arg Leu Ser Ser
 180 185 190
 Asp Gly Lys Gln Ile Ile Ile Thr Ala Thr Met Met Gly Thr Ala Ile
 195 200 205
 Asn Pro Lys Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys
 210 215 220
 Thr Leu Asp Cys Gly Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile Phe
 225 230 235 240
 Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe
 245 250 255
 Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn
 260 265 270
 Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly
 275 280 285

Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser
 290 295 300
 Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn Ile
 305 310 315 320
 Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg
 325 330 335
 Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser
 340 345 350
 Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu
 355 360 365
 Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe
 370 375 380
 Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe
 385 390 395 400
 Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile Asn
 405 410 415
 Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile Asn
 420 425 430
 Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly
 435 440 445
 Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp Phe
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 Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe
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 Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn Asp
 485 490 495
 Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn
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 Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg Arg
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Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr
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Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn
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Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala Ile
580 585 590

Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln
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Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys
610 615 620

Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr
625 630 635 640

Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu Val
645 650 655

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Thr His Trp Gly Phe Val Pro Val Ser Glu
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Cys Ser Ala Ile Glu Gly Arg Ala Pro Gly Ile Cys
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<400> 17

Cys Gly Ile Glu Gly Arg Ala Pro Gly Pro Gly Ser Ser Val Gly Ser
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Ser Leu Ser Cys
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<210> 18
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<400> 18

Cys Gly Leu Val Pro Arg Gly Ser Gly Pro Cys
 1 5 10

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<400> 19

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Ser Leu Ser Cys
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<210> 20
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 <220>
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<400> 20

Cys Lys Ser Asp Asp Asp Asp Lys Ala Pro Gly Ile Cys
 1 5 10

<210> 21
 <211> 22
 <212> PRT
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<400> 21

Cys Lys Ser Glu Glu Lys Leu Tyr Asp Asp Asp Asp Lys Asp Arg Trp
 1 5 10 15

Gly Ser Ser Arg Ile Cys
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<210> 22
 <211> 17

<212> PRT
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 <400> 22

Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn Lys Thr Leu Asp
 1 5 10 15

Cys

<210> 23
 <211> 10
 <212> PRT
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<400> 23

Cys Gly Leu Val Pro Ala Gly Ser Gly Pro
 1 5 10

<210> 24
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<400> 24

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 1 5 10 15

Cys

<210> 25
 <211> 10
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<400> 25

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10

<210> 26
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 <212> PRT
 <213> Artificial Sequence
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<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 27

Pro Pro Pro Ile Glu Gly Arg
 1 5

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)	
)	
Clifford Charles Shone et al.)	
)	
International Application No. PCT/GB03/03082)	Examiner: Brian J. Gangle
)	
Application No.: 10/521,401)	Group Art Unit: 1645
)	
International Filing Date: July 15, 2003)	Confirmation No.: 2849

For **TARGETED AGENTS FOR NERVE
REGENERATION**

STATEMENT ACCORDING TO 37 C.F.R. § 1.821(f)


M.S. – SEQUENCE LISTING
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

Submitted herewith is a sequence listing as part of the above-captioned patent application. Applicants' representative states that the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are identical.

Applicants' representative hereby verifies that the information on the accompanying computer readable copy is identical to the paper copy of the sequence listing. The enclosed sequence listing does not include any new matter that goes beyond the disclosure in the above-captioned application as filed.

Respectfully submitted,


Daniel W. Celandor, Ph.D.
Registration No. 52,710

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